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## RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/10/051,909

TIME: 12:40:00

Input Set : A:\BB1163 US CIP Seq Listing.txt

Output Set: N:\CRF3\02072002\J051909.raw

2 <110> APPLICANT: Allen, Steve  
3 Helentjaris, Tim  
4 Hitz, Bill  
5 Kinney, Tony  
6 Tingey, Scott  
8 <120> TITLE OF INVENTION: Plant Sugar Transport Proteins  
10 <130> FILE REFERENCE: BB1163 US CIP  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/051,909  
C--> 13 <141> CURRENT FILING DATE: 2002-01-17  
15 <150> PRIOR APPLICATION NUMBER: 60/083,044  
W--> 16 <151> PRIOR FILING DATE: April 24, 1998  
18 <160> NUMBER OF SEQ ID NOS: 38  
20 <170> SOFTWARE: Microsoft Office 97  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 2824  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Zea mays  
27 <220> FEATURE:  
28 <221> NAME/KEY: unsure  
29 <222> LOCATION: (29)  
31 <220> FEATURE:  
32 <221> NAME/KEY: unsure  
33 <222> LOCATION: (622)  
35 <220> FEATURE:  
36 <221> NAME/KEY: unsure  
37 <222> LOCATION: (636)  
39 <220> FEATURE:  
40 <221> NAME/KEY: unsure  
41 <222> LOCATION: (638)  
43 <220> FEATURE:  
44 <221> NAME/KEY: unsure  
45 <222> LOCATION: (669)  
47 <220> FEATURE:  
48 <221> NAME/KEY: unsure  
49 <222> LOCATION: (771)  
51 <220> FEATURE:  
52 <221> NAME/KEY: unsure  
53 <222> LOCATION: (822)  
55 <220> FEATURE:  
56 <221> NAME/KEY: unsure  
57 <222> LOCATION: (856)  
59 <220> FEATURE:  
60 <221> NAME/KEY: unsure

ENTERED

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Input Set : A:\BB1163 US CIP Seq Listing.txt

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61 <222> LOCATION: (889)  
 63 <220> FEATURE:  
 64 <221> NAME/KEY: unsure  
 65 <222> LOCATION: (896)  
 67 <220> FEATURE:  
 68 <221> NAME/KEY: unsure  
 69 <222> LOCATION: (944)  
 71 <400> SEQUENCE: 1

W--> 72 cccaccccc tccactccac taccacggng gcacggcctg cctctgcagc tctgccctgc 60  
 73 tccgcacccc tcgctctcca accccaacgc gcggcgctgc taaaattcac ctcagcgcggt 120  
 74 actccagttt ggccacctca ccaccgcgcg ccgctgttta agaaggcccc gcgcccgatc 180  
 75 ggggatcacg aaccttgccc gccgctgccg gagggtgggc gtagatttcc ggcgccatg 240  
 76 gggggcgccg tgatggctgc catcgcgccc tctatcgcca acttgctgca gggctgggac 300  
 77 aatgcgacaa ttgctggagc cgtcctgtac ataaagaagg aattcaacct gcagagcgag 360  
 78 cctctgatcg aaggcctcat cgtcgccatg ttcctcattg gggcaacagt catcacaaca 420  
 79 tctccggggc caagggctga ctgcgttggt aggaggccca tgctggctgc ctcggtctgc 480  
 80 ctctacttgc tcagtgggct ggtgatgctt tgggcgcca ttgtgtacat cttgctcctc 540  
 81 gcaaggctca ttgatgggtt cggtatcggt ttggcggtca caettgttcc tctctacatc 600  
 W--> 82 tccgaaactg caccgcacag ahattcttgg ggctgntnga acacgttgcc gcagttcatt 660  
 W--> 83 ggggtcagng gagggatgtt cctctcctac tgcattggtg ttgggatgtc cctcatgccc 720  
 W--> 84 aaacctgatt ggaggtcat gcttgagatt ctgtcgatcc cgctacttat ntactttgga 780  
 W--> 85 ctgactgtct tctacttgcc tgaatcacca aggtggcttg tnagcaaagg aaggatggcg 840  
 W--> 86 gaggcgaaga gagtgtgca aaggctgcgg ggaagagaag atgtctcang ggaganngct 900  
 W--> 87 cttctagttg aaggtttggg ggtcggtaaa gatacacgta ttttagagta catcattgga 960  
 88 cctgccaccg aggcagccga tgatcttgta actgacggtg ataaggaaca aatcacactt 1020  
 89 tatgggcctg aagaaggcca gtcattgatt gctcgacctt ctaagggacc catcatgctt 1080  
 90 ggaagtgtgc tttctcttgc atctcgtcat gggagcatgg tgaaccagag tgtaacctt 1140  
 91 atggatccga ttgtgacact ttttggtagt gtccatgaga atatgcctca agctggagga 1200  
 92 agtatgagga gcacattgtt tccaaacttt ggaagtatgt tcagtgtcac agatcagcat 1260  
 93 gccaaaaatg agcagtggga tgaagagaat cttcataggg atgacgagga gtacgcatct 1320  
 94 gatggtgcag gagggtgacta tgaggacaat ctccatagcc cattgctgtc caggcaggca 1380  
 95 acaggtgcgg aagggaagga cattgtgcac catggtcacc gtggaagtgc tttgagcatg 1440  
 96 agaaggcaaa gcctcttagg ggaggggtgga gatggtgtga gcagcactga tatcggtggg 1500  
 97 ggatggcagc ttgcttgtaa atggtcagag aaggaaggtg agaattgtag aaaggaaggt 1560  
 98 ggtttcaaaa gagtctactt gcaccaagag ggagttcctg gctcaagaag gggctcaatt 1620  
 99 gtttcacttc ccggtgggtg cgatgttctt gagggtagtg agtttgtaca tgctgctgct 1680  
 100 ttagtaagtc agtcagcact tttctcaaag ggtcttgctg aaccacgcat gtcagatgct 1740  
 101 gccatggttc acccatctga ggtagctgcc aaaggttcac gttggaaaga tttgtttgaa 1800  
 102 cctggagtga ggcggtccct gttagctcgt gttggaattc agatccttca acagtttgct 1860  
 103 ggaataaacg gtgttctgta ctatacccca caaattcttg agcaagctgg tgtggcagtt 1920  
 104 attctttcca aatttgggtc cagctcgcca tcagcatcca tcttgatcag ttctctcact 1980  
 105 accttactaa tgcttccttg cattggcttt gccatgctgc ttatggatct tccgggaaga 2040  
 106 aggtttttgc tgctaggcac aattccaatc ttgatagcat ctctagttat cctggttggt 2100  
 107 tccaatctaa ttgatttggt tacactagcc catgctttgc tctccaccat cagtgttatc 2160  
 108 gtctacttct gctggttctg tatgggattt ggtcccatcc ccaacatttt atgtgcagag 2220  
 109 atctttccaa ccagggttcg tggcctctgt attgccattt gtgcctttac attctggatc 2280  
 110 ggagatatca tcgtcaccta cagccttctt gtgatgctga atgctatttg actggcgggt 2340  
 111 gttttcagca tatatgcagt cgtatgcttg atttcttttg tgttcgtctt ccttaagggtc 2400  
 112 cctgagacaa aggggatgcc ccttgaggtt attaccgaat tctttgcagt tgggtcggaag 2460

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Input Set : A:\BB1163 US CIP Seq Listing.txt

Output Set: N:\CRF3\02072002\J051909.raw

```

113 caagcggctg caaaagccta atttctttgg tacctttgtg tgcaactatt gcactgtaag 2520
114 ttagaaactt gaaggggttt caccaagaag ctcgagagaat tactttggat ttgtgtaaat 2580
115 gttaaggga cgaacatctg ctcatgctcc tcaaacggta aaaaagagtc cctcaatggc 2640
116 aaataggagt cgtaagtgt tcaatgtcat ttaccatag ttttacctat ttgtactgta 2700
117 ttataagtca agctattcaa cgctggttgt tgctagaaat ctttagaaca aagatgataa 2760
118 tgatctgata tgatgttata atattcaaat ctcaaataaa gaaaatatcg tttctcaaaa 2820
119 aaaa 2824
121 <210> SEQ ID NO: 2
122 <211> LENGTH: 747
123 <212> TYPE: PRT
124 <213> ORGANISM: Zea mays
126 <220> FEATURE:
127 <221> NAME/KEY: UNSURE /
128 <222> LOCATION: (129)
130 <220> FEATURE:
131 <221> NAME/KEY: UNSURE
132 <222> LOCATION: (133)..(134)
134 <220> FEATURE:
135 <221> NAME/KEY: UNSURE
136 <222> LOCATION: (144) /
138 <220> FEATURE:
139 <221> NAME/KEY: UNSURE
140 <222> LOCATION: (178) /
142 <220> FEATURE:
143 <221> NAME/KEY: UNSURE
144 <222> LOCATION: (207) /
146 <220> FEATURE:
147 <221> NAME/KEY: UNSURE
148 <222> LOCATION: (218) /
150 <220> FEATURE:
151 <221> NAME/KEY: UNSURE
152 <222> LOCATION: (220) /
154 <220> FEATURE:
155 <221> NAME/KEY: UNSURE
156 <222> LOCATION: (236) /
158 <400> SEQUENCE: 2
159 Met Gly Gly Ala Val Met Val Ala Ile Ala Ala Ser Ile Gly Asn Leu
160 1 5 10 15
162 Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val Leu Tyr Ile
163 20 25 30
165 Lys Lys Glu Phe Asn Leu Gln Ser Glu Pro Leu Ile Glu Gly Leu Ile
166 35 40 45
168 Val Ala Met Phe Leu Ile Gly Ala Thr Val Ile Thr Thr Ser Pro Gly
169 50 55 60
171 Pro Arg Ala Asp Cys Val Gly Arg Arg Pro Met Leu Val Ala Ser Ala
172 65 70 75 80
174 Val Leu Tyr Phe Val Ser Gly Leu Val Met Leu Trp Ala Pro Ile Val
175 85 90 95
177 Tyr Ile Leu Leu Leu Ala Arg Leu Ile Asp Gly Phe Gly Ile Gly Leu

```

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```

178          100          105          110
180 Ala Val Thr Leu Val Pro Leu Tyr Ile Ser Glu Thr Ala Pro His Arg
181          115          120          125
W--> 183 Xaa Ser Trp Gly Xaa Xaa Asn Thr Leu Pro Gln Phe Ile Gly Val Xaa
184          130          135          140
186 Gly Gly Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met
187 145          150          155          160
189 Pro Lys Pro Asp Trp Arg Leu Met Leu Gly Val Leu Ser Ile Pro Ser
190          165          170          175
W--> 192 Leu Xaa Tyr Phe Gly Leu Thr Val Phe Tyr Leu Pro Glu Ser Pro Arg
193          180          185          190
W--> 195 Trp Leu Val Ser Lys Gly Arg Met Ala Glu Ala Lys Arg Val Xaa Gln
196          195          200          205
W--> 198 Arg Leu Arg Gly Arg Glu Asp Val Ser Xaa Glu Xaa Ala Leu Leu Val
199          210          215          220
W--> 201 Glu Gly Leu Gly Val Gly Lys Asp Thr Arg Ile Xaa Glu Tyr Ile Ile
202 225          230          235          240
204 Gly Pro Ala Thr Glu Ala Ala Asp Asp Leu Val Thr Asp Gly Asp Lys
205          245          250          255
207 Glu Gln Ile Thr Leu Tyr Gly Pro Glu Gly Gln Ser Trp Ile Ala
208          260          265          270
210 Arg Pro Ser Lys Gly Pro Ile Met Leu Gly Ser Val Leu Ser Leu Ala
211          275          280          285
213 Ser Arg His Gly Ser Met Val Asn Gln Ser Val Pro Leu Met Asp Pro
214          290          295          300
216 Ile Val Thr Leu Phe Gly Ser Val His Glu Asn Met Pro Gln Ala Gly
217 305          310          315          320
219 Gly Ser Met Arg Ser Thr Leu Phe Pro Asn Phe Gly Ser Met Phe Ser
220          325          330          335
222 Val Thr Asp Gln His Ala Lys Asn Glu Gln Trp Asp Glu Glu Asn Leu
223          340          345          350
225 His Arg Asp Asp Glu Glu Tyr Ala Ser Asp Gly Ala Gly Gly Asp Tyr
226          355          360          365
228 Glu Asp Asn Leu His Ser Pro Leu Leu Ser Arg Gln Ala Thr Gly Ala
229          370          375          380
231 Glu Gly Lys Asp Ile Val His His Gly His Arg Gly Ser Ala Leu Ser
232 385          390          395          400
234 Met Arg Arg Gln Ser Leu Leu Gly Glu Gly Asp Gly Val Ser Ser
235          405          410          415
237 Thr Asp Ile Gly Gly Gly Trp Gln Leu Ala Trp Lys Trp Ser Glu Lys
238          420          425          430
240 Glu Gly Glu Asn Gly Arg Lys Glu Gly Gly Phe Lys Arg Val Tyr Leu
241          435          440          445
243 His Gln Glu Gly Val Pro Gly Ser Arg Arg Gly Ser Ile Val Ser Leu
244          450          455          460
246 Pro Gly Gly Gly Asp Val Leu Glu Gly Ser Glu Phe Val His Ala Ala
247 465          470          475          480
249 Ala Leu Val Ser Gln Ser Ala Leu Phe Ser Lys Gly Leu Ala Glu Pro
250          485          490          495

```

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```

252 Arg Met Ser Asp Ala Ala Met Val His Pro Ser Glu Val Ala Ala Lys
253          500          505          510
255 Gly Ser Arg Trp Lys Asp Leu Phe Glu Pro Gly Val Arg Arg Ala Leu
256          515          520          525
258 Leu Val Gly Val Gly Ile Gln Ile Leu Gln Gln Phe Ala Gly Ile Asn
259          530          535          540
261 Gly Val Leu Tyr Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Ala
262 545          550          555          560
264 Val Ile Leu Ser Lys Phe Gly Leu Ser Ser Ala Ser Ala Ser Ile Leu
265          565          570          575
267 Ile Ser Ser Leu Thr Thr Leu Leu Met Leu Pro Cys Ile Gly Phe Ala
268          580          585          590
270 Met Leu Leu Met Asp Leu Ser Gly Arg Arg Phe Leu Leu Leu Gly Thr
271          595          600          605
273 Ile Pro Ile Leu Ile Ala Ser Leu Val Ile Leu Val Val Ser Asn Leu
274          610          615          620
276 Ile Asp Leu Gly Thr Leu Ala His Ala Leu Leu Ser Thr Ile Ser Val
277 625          630          635          640
279 Ile Val Tyr Phe Cys Cys Phe Val Met Gly Phe Gly Pro Ile Pro Asn
280          645          650          655
282 Ile Leu Cys Ala Glu Ile Phe Pro Thr Arg Val Arg Gly Leu Cys Ile
283          660          665          670
285 Ala Ile Cys Ala Phe Thr Phe Trp Ile Gly Asp Ile Ile Val Thr Tyr
286          675          680          685
288 Ser Leu Pro Val Met Leu Asn Ala Ile Gly Leu Ala Gly Val Phe Ser
289          690          695          700
291 Ile Tyr Ala Val Val Cys Leu Ile Ser Phe Val Phe Val Phe Leu Lys
292 705          710          715          720
294 Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe
295          725          730          735
297 Ala Val Gly Ala Lys Gln Ala Ala Ala Lys Ala
298          740          745
300 <210> SEQ ID NO: 3
301 <211> LENGTH: 443
302 <212> TYPE: DNA
303 <213> ORGANISM: Oryza sativa
305 <220> FEATURE:
306 <221> NAME/KEY: unsure
307 <222> LOCATION: (193)
309 <220> FEATURE:
310 <221> NAME/KEY: unsure
311 <222> LOCATION: (388)
313 <220> FEATURE:
314 <221> NAME/KEY: unsure
315 <222> LOCATION: (435)
317 <220> FEATURE:
318 <221> NAME/KEY: unsure
319 <222> LOCATION: (439)
321 <400> SEQUENCE: 3

```

Show sequence in bold letters and italics  
 Turn on/off sequence in bold letters and italics  
 Turn on/off sequence in bold letters and italics  
 Turn on/off sequence in bold letters and italics

## VERIFICATION SUMMARY

DATE: 02/07/2002

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Input Set : A:\BB1163 US CIP Seq Listing.txt

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L:12 M:270 C: Current Application Number differs, Replaced Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:72 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:82 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:83 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:84 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:84 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:85 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:86 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:87 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:183 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:192 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:195 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:198 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:201 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:325 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:328 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:329 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:357 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:369 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:801 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:802 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:1053 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:1053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1055 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:1055 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1056 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:1056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1058 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17

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Input Set : A:\BB1163 US CIP Seq Listing.txt

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L:1058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1060 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:1060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1061 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1095 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:1095 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1104 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:1104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1116 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:1116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1335 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22  
L:1335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:2632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36